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functions of proteome. It is thus very important to group the proteins contained in a biological sample based on some idea before proteome analysis and some attempts at pretreatment has been made up to this day. For example, Molly et al. [Eur. J. Biochem. 267, 2871-2881 (2000)] and Santoni et al. [Electrophoresis 21, 1054-1070 (2000)] pretreated a sample with strong solubilizer, but have not solubilized all proteins. Herbert et al. [Electrophoresis 21, 3639-3648 (2000)] and Zuo et al. [Anal. Biochem. 284, 266-278 (2000)] pretreated samples by separating depending on their isoelectric point, but it is difficult to set appropriate range of isoelectric point for target proteins, and isoelectric focusing was prevented. It should be noted that these attempts are aiming at partial improvement of electrophoresis method, and not aiming at total proteome analysis of by grouping total proteome realized by this invention. To date, however, since no effective idea of grouping has been proposed, the same methods are employed from sample preparation to the analysis thereafter, without grouping samples. This forces the proteomic study to encounter the above-mentioned two problems.

IN THE CLAIMS:

6. (Amended) A proteome analysis device comprising at least the following

devices:

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- (a) a device for transferring an analyte including compounds capable of interacting with membrane proteins from an electrophoresed gel onto a support for immobilizing the compounds while retaining the native function of said compounds;
- (b) a device for preparing a lipid bilayer for embedding the membrane proteins;
- (c) a device for trapping the membrane proteins embedded in the lipid bilayer, which are capable of interacting with the compounds immobilized on the support, by bringing said membrane proteins in contact with said compounds;
- (d) a device for obtaining at least a piece of physical or chemical information of both or each of said membrane proteins and said compounds.

15. (New) A library of membrane proteins embedded in liposome.

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